



SEQUENCE LISTING

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NeuroMed Technologies, Inc.

<120> NOVEL HUMAN CALCIUM CHANNELS AND RELATED
PROBES, CELL LINES AND METHODS

<130> 38109-20007.00

<140> US 09/030,482
<141> 1998-02-25

<150> US 60/039,204
<151> 1997-02-28

<160> 33

<170> FastSEQ for Windows Version 4.0

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<210> 13
<211> 168
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tacaacttca tctacttcat cctgcttATC ataccCCTCT tgcCTTgcac cccatATggT
120
cttcccAGAG tgagctcatc cacctcgtca tgcCTgactc gacgttca
168

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<211> 98
<212> DNA
<213> Human

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cgtcctgagg cccctcaaag ccatcaacccg cgtgccca
98

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<211> 94
<212> DNA
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120
agg
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120
caaaggggat ccgcacgctg ctcttgctt ttagatgttc cttccctgcg ttgttaaca
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tcggncctt tctttcctg gtcatgttca tctacgnat cttggatg tccaattttg
240
cctatgttaa gagggaaagtt gggatcgatg acatgttnan cttgagacc tttggcaaca
300
gcatgatctg cctgttccaa attacaacct ctgctggctg gga
343

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<222> (1)...(5562)
<223> Human alpha-1 partial sequence from BAC bk206c7

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48
Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp
1 5 10 15

tta aac gtg gcc aat atg gac aac ttc ttc gcc ccc gtt ttc acc atg
96
Leu Asn Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met
20 25 30

ggc aaa tat tat acg caa ggc gac aag gtg ctg atg ccg ctg gcg att
144
Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
35 40 45

cag gct ctg aaa cag ctg atg ttc aaa ttg gtg gcc act gtt gct cga
192
Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg
50 55 60

aca cat gct aca ccg tca cac atc acg ggt ggt cct gga aca ggg atg
240
Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met
65 70 75 80

cac acg ggc acc ttc cag gaa gga gct gag cct ggt tca tct cag cac
288
His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His
85 90 95

cct gag gca cag gcc acg tat aca gca ggg tgc acc cca gcc ccc acg
336
Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr
100 105 110

ggc gat ccc acc tgc tgc ttt gtc ctt gac ttg gtg tgc acg tgg ttt
384
Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe
115 120 125

gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt ggc
432
Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly
130 135 140

atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc aag
480
Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys
145 150 155 160

atc ctg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg gag
528
Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu
165 170 175

atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc tac
576

Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr
180 185 190
ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca ggc
624
Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly
195 200 205
aac atc aac ctg tca gcc atc cgc acc gtg cgc gtc ctg agg ccc ctc
672
Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
210 215 220
aaa gcc atc aac cgc gtg ccc agt atg cgg atc ctg gtg aac ctg ctc
720
Lys Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu
225 230 235 240
ctg gac aca ctg ccc atg ctg ggg aat gtc ctg ctg ctc tgc ttc ttt
768
Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe
245 250 255
gtc ttc ttc atc ttt ggc atc ata ggt gtg cag ctc tgg gcg ggc ctg
816
Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu
260 265 270
ctg cgt aac cgc tgc ttc ctg gag gag aac ttc acc ata caa ggg gat
864
Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp
275 280 285
gtg gcc ttg ccc cca tac tac cag ccg gag gag gat gat gat atg ccc
912
Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro
290 295 300
ttc atc tgc tcc ctg tcg ggc gac aat ggg ata atg ggc tgc cat gag
960
Phe Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met Gly Cys His Glu
305 310 315 320
atc ccc ccg ctc aag gag cag ggc cgt gag tgc tgc ctg tcc aag gac
1008
Ile Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp
325 330 335
gac gtc tac gac ttt ggg gcg ggg cgc cag gac ctc aat gcc agc ggc
1056
Asp Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly
340 345 350
ctc tgt gtc aac tgg aac cgt tac tac aat gtg tgc cgc acg ggc agc
1104
Leu Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser
355 360 365

gcc aac ccc cac aag ggt gcc atc aac ttt gac aac atc ggt tat gct
1152
Ala Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala
370 375 380

tgg att gtc atc ttc cag gtg atc act ctg gaa ggc tgg gtg gag atc
1200
Trp Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile
385 390 395 400

atg tac tac gtg atg gat gct cac tcc ttc tac aac ttc atc tac ttc
1248
Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe
405 410 415

atc ctg ctt atc ata agt gag ctc atc cac ctc gtc atg cct gac tgc
1296
Ile Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys
420 425 430

agc ttc agc aca gca cag tcc cca aaa tgt caa ggt gat tca ctc cca
1344
Ser Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro
435 440 445

gga gtc gct gct gaa tcc ctg ctg cga gac tct agc tcc tca gtc
1392
Gly Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Val
450 455 460

atc act gat gag gct gca gcc atg gag aac ctc ctg gcg ggc acc tcc
1440
Ile Thr Asp Glu Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser
465 470 475 480

aag ggg gat gaa agc tat ctg ctc agg ctg gcc ggc agc caa gtt cac
1488
Lys Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His
485 490 495

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1536
Ser Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu
500 505 510

gaa act gga gag gag ccc cac tcg tgg agc cct cgg gcc aca agg aga
1584
Glu Thr Gly Glu Glu Pro His Ser Trp Ser Pro Arg Ala Thr Arg Arg
515 520 525

tgg gat ccc caa tgc caa cca ggg cag cct ctc ccc ctt cat ttc atg
1632
Trp Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu Pro Leu His Phe Met
530 535 540

caa gca cag gtg ggc tcc ttc atg atc aac ctg tgc ctc gtt gtc
1680
Gln Ala Gln Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
545 550 555 560

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1728
Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met
565 570 575

ctg gag cag cgg cag cgc tac ctg tcc tcc agc acg gtg gcc agc tac
1776
Leu Glu Gln Arg Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr
580 585 590

gcc gag cct ggc gac tgc tac gag gag atc ttc cag tat gtc tgc cac
1824
Ala Glu Pro Gly Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His
595 600 605

atc ctg cgc aag gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg
1872
Ile Leu Arg Lys Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu
610 615 620

cag agc cgg cgc cag gcc ctg ggc ccc gag gcc ccc ccc gcc aaa
1920
Gln Ser Arg Arg Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys
625 630 635 640

cct ggg ccc cac gcc aag gag ccc cgg cac tac cct ctc aca gtc tgg
1968
Pro Gly Pro His Ala Lys Glu Pro Arg His Tyr Pro Leu Thr Val Trp
645 650 655

gaa tcg att ctt ggg agg caa gca gaa gaa tgc acg ctc aga gct gcc
2016
Glu Ser Ile Leu Gly Arg Gln Ala Glu Glu Cys Thr Leu Arg Ala Ala
660 665 670

gcc cac ccg tcc tcg ggt gcc agc cat cca ggc gtg ggc tcg gag gag
2064
Ala His Pro Ser Ser Gly Ala Ser His Pro Gly Val Gly Ser Glu Glu
675 680 685

gcc cca gag ctg tgc ccg caa cat agc ccc ctg gat gcg acg ccc cac
2112
Ala Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr Pro His
690 695 700

acc ctg gtg cag ccc atc ccc gcc acg ctg gct tcc gat ccc gcc agc
2160
Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser
705 710 715 720

tgc cct tgc tgc cag cat gag gac ggc cgg ccc tcg ggc ctg ggc
2208

Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly
725 730 735
agc acc gac tcg ggc cag gag ggc tcg ggc tcc ggg agc tcc gct ggt
2256
Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Ser Ala Gly
740 745 750
ggc gag gac gag gcg gat ggg gac ggg gcc cg^g agc agc gag gac gga
2304
Gly Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly
755 760 765
gcc tcc tca gaa ctg ggg aag gag gag gag gag gag cag gcg gat
2352
Ala Ser Ser Glu Leu Gly Lys Glu Glu Glu Glu Gln Ala Asp
770 775 780
ggg gcg gtc tgg ctg tgc ggg gat gtg tgg cg^g gag acg cga gcc aag
2400
Gly Ala Val Trp Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Ala Lys
785 790 795 800
ctg cgc ggc atc gtg gac agc aag tac ttc aac cg^g ggc atc atg atg
2448
Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met
805 810 815
gcc atc ctg gtc aac acc gtc agc atg ggc atc gag cac cac gag cag
2496
Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln
820 825 830
gcc agt gca gcg cag ccg ggc cg^g gcc tgc ggg aga gga caa aat cca
2544
Ala Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln Asn Pro
835 840 845
gac ctt tgc atg acc ctc aag gcc cct tgt ctc tgt cac aac gtc cct
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Asp Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro
850 855 860
tca cca ggc cag ggt gtc ctg tcc cat cca gtg act cca ccc cat aca
2640
Ser Pro Gly Gln Gly Val Leu Ser His Pro Val Thr Pro Pro His Thr
865 870 875 880
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2688
Ala Pro Trp Arg Met Glu Thr Gly Lys Gln Gly His Gly Cys Glu Glu
885 890 895
gga cca gga caa cga agc agt gac atg ttt gcc ctg gag atg atc ctg
2736
Gly Pro Gly Gln Arg Ser Ser Asp Met Phe Ala Leu Glu Met Ile Leu
900 905 910

aag ctg gct gca ttt ggg ctc ttc gac tac ctg cgt aac ccc tac aac
2784
Lys Leu Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn
915 920 925

atc ttc gac agc atc att gtc atc atc agc atc tgg gag atc gtg ggg
2832
Ile Phe Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly
930 935 940

cag gcg gac ggt ggg ctg tcg gtg ctg cgg acc ttc cgg ctg ctg cgc
2880
Gln Ala Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg
945 950 955 960

gtg ctg aaa ctg gtg cgc ttc atg cct gcc ctg cgg cgc cag ctc gtg
2928
Val Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val
965 970 975

gtg ctc atg aag acc atg gac aac gtg gcc acc ttc tgc atg ctg ctc
2976
Val Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu
980 985 990

atg ctc ttc atc ttc atc agc atc ctt ggg atg cat att ttt ggc
3024
Met Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly
995 1000 1005

tgc aag ttc agc ctc cgc acg gac act gga gac acg gtg ccc gac agg
3072
Cys Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg
1010 1015 1020

aag aac ttc gac tcc ctg ctg tgg gcc atc gtc act gtg ttc cag atc
3120
Lys Asn Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile
1025 1030 1035 1040

ctc acc cag gag gac tgg aac gtc gtt ctc tac aat ggc atg gcc tcc
3168
Leu Thr Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser
1045 1050 1055

act tct ccc tgg gcc tcc ctc tac ttt gtc gcc ctc atg acc ttc ggc
3216
Thr Ser Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly
1060 1065 1070

aac tat gtg ctc ttc aac ctg ctg gtg gcc atc ctg gtg gag ggc ttc
3264
Asn Tyr Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe
1075 1080 1085

cag gcg gag gtg act gtg gtc ttg gca gag gaa gca ccc cca cag ggc
3312
Gln Ala Glu Val Thr Val Val Leu Ala Glu Glu Ala Pro Pro Gln Gly
1090 1095 1100

ctg cga aag act ggg cga ggg aga ggt ggc ctg gat ggg gga ggg ctg
3360
Leu Arg Lys Thr Gly Arg Gly Arg Gly Leu Asp Gly Gly Leu
1105 1110 1115 1120

caa ttc aaa ctt cta gca ggc aac cta tcc cta aag gag ggg gtt gct
3408
Gln Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly Val Ala
1125 1130 1135

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3456
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1140 1145 1150

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3504
Ser Ser Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser
1155 1160 1165

agc gga gat ccc aag ctc tgc cca atc ccc atg acc ccc aat ggg cac
3552
Ser Gly Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His
1170 1175 1180

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3600
Leu Asp Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala
1185 1190 1195 1200

gcg gga cct gcc ccc cga ctc tca ctg cag ccg gac ccc atg ctg gtg
3648
Ala Gly Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val
1205 1210 1215

gcc ctg ggc tcc cga aag agc agc gtc atg tct cta ggg agg atg agc
3696
Ala Leu Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser
1220 1225 1230

tat gac cag cgc tcc ctg gtg ggt ctt aga gcc aca gcg ggg gtg
3744
Tyr Asp Gln Arg Ser Leu Val Gly Gly Leu Arg Ala Thr Ala Gly Val
1235 1240 1245

cag gct gcc ttt ggg cac ctg gtg ccc cag ccg tgg gtg tgc ctg tgg
3792
Gln Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp Val Cys Leu Trp
1250 1255 1260

ggc gct gac ccg aac ggg aac tcc ttc cag tcc agc tcc cgg agc tcc
3840

Gly Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg Ser Ser
1265 1270 1275 1280

tac tac ggg cca tgg ggc cgc agc gcg gcc tgg gcc agc cgt cgc tcc
3888

Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser
1285 1290 1295

agc tgg aac agc ctc aag cac aag ccg ccg tcg gcg gag cat gag tcc
3936

Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser
1300 1305 1310

ctg ctc tct gcg gag cgc ggc ggc ggc gcc cgg gtc tgc gag gtt gcc
3984

Leu Leu Ser Ala Glu Arg Gly Gly Ala Arg Val Cys Glu Val Ala
1315 1320 1325

gcg gac gag ggg ccg ccg cgg gca ccc ctg cac acc cca cac gcc
4032

Ala Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala
1330 1335 1340

cac cac gtt cat cac ggg ccc cat ctg gcg cac cgc cac cgc cac
4080

His His Val His His Gly Pro His Leu Ala His Arg His Arg His His
1345 1350 1355 1360

cgc cgg acg ctg tcc ctc gac aac agg gac tcg gtg gac ctg gcc gag
4128

Arg Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser Val Asp Leu Ala Glu
1365 1370 1375

ctg gtg ccc gcg gtg ggc gcc cac ccc cgg gcc gac tgg agg gca
4176

Leu Val Pro Ala Val Gly Ala His Pro Arg Ala Ala Trp Arg Ala Ala
1380 1385 1390

ggc ccg gcc ccc ggg cat gag gac tgc aat ggc agg atg ccc agc atc
4224

Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile
1395 1400 1405

gcc aaa gac gtc ttc acc aag atg ggc gac cgc ggg gat cgc ggg gag
4272

Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg Gly Glu
1410 1415 1420

gat gag gag gaa atc gac tac gtg agt ggg ggc ggg gac gaa ggg gag
4320

Asp Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Ala Glu Gly Asp
1425 1430 1435 1440

ctg acc ctg tgc ttc cgc gtc cgc aag atg atc gac gtc tat aag ccc
4368

Leu Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro
1445 1450 1455

gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc
 4416
 Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro
 1460 1465 1470

 gag aac agg ctc agg gat ctg ggc tgg gta agc ctc gag tgc cag gga
 4464
 Glu Asn Arg Leu Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly
 1475 1480 1485

 aag gtg ggt gac ctc gtg gtg tgg tat ggt cag agg agg cag cgc
 4512
 Lys Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg
 1490 1495 1500

 cag acc att att gcc cac aaa ctc ttc gac tac gtc gtc ctg gcc ttc
 4560
 Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe
 1505 1510 1515 1520

 atc ttt ctc aac tgc atc acc atc gcc ctg gag cgg cct cag atc gag
 4608
 Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu
 1525 1530 1535

 gcc ggc agc acc gaa cgc atc ttt ctc acc gtg tcc aac tac atc ttc
 4656
 Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe
 1540 1545 1550

 acg gcc atc ttc gtg ggc gag atg aca ttg aag gta gtc tcg ctg ggc
 4704
 Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly
 1555 1560 1565

 ctg tac ttc ggc gag cag gcg tac cta cgc agc agc tgg aac gtg ctg
 4752
 Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
 1570 1575 1580

 gat ggc ttt ctt gtc ttc gtg tcc atc atc gac atc gtg gtg tcc ctg
 4800
 Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu
 1585 1590 1595 1600

 gcc tca gcc ggg gga gcc aag atc ttg ggg gtc ctc cga gtc ttg cgg
 4848
 Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg
 1605 1610 1615

 ctc ctg cgc acc cta cgc ccc ctg cgt gtc atc agc cgg gcg ccg ggc
 4896
 Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly
 1620 1625 1630

ctg aag ctg gtg gag aca ctc atc tcc tcc ctc aag ccc atc ggc
4944
Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly
1635 1640 1645

aac atc gtg ctc atc tgc tgt gcc ttc ttc atc atc ttt ggc atc ctg
4992
Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
1650 1655 1660

gga gtg cag ctc ttc aag ggc aag ttc tac cac tgt ctg ggc gtg gac
5040
Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp
1665 1670 1675 1680

acc cgc aac atc acc aac cgc tcg gac tgc atg gcc gcc aac tac cgc
5088
Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Met Ala Ala Asn Tyr Arg
1685 1690 1695

tgg gtc cat cac aaa tac aac ttc gac aac ctg ggc cag gct ctg atg
5136
Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
1700 1705 1710

tcc ctc ttt gtc ctg gca tcc aag gat ggt tgg gtg aac atc atg tac
5184
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr
1715 1720 1725

aat gga ctg gat gct gtt gtg gac cag cag cct gtg acc aac cac
5232
Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His
1730 1735 1740

aac ccc tgg atg ctg ctg tac ttc atc tcc ttc ctg ctc atc gtc agc
5280
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser
1745 1750 1755 1760

ttc ttt gtg ctc aac atg ttt gtg ggt gtc gtg gtg gag aac ttc cac
5328
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1765 1770 1775

aag tgc cgg cag cac cag gag gct gaa gag gca cgg cgg cgt gag gag
5376
Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu
1780 1785 1790

aag cgg ctg cgg cgc ctg gag aag aag cgc cgg aag gcc cag cgg ctg
5424
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu
1795 1800 1805

ccc tac tat gcc acc tat tgt cac acc cgg ctg ctc atc cac tcc atg
5472

Pro Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met
 1810 1815 1820
 tgc acc agc cac tac ctg gac atc ttc atc acc ttc atc atc tgc ctc
 5520
 Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu
 1825 1830 1835 1840
 aac gtg gtc acc atg tcc ctg gag cac tac aat cag ccc acg
 5562
 Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
 1845 1850

<210> 19
 <211> 1853
 <212> PRT
 <213> Human

<400> 19
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 1 5 10 15
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 20 25 30
 Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln
 35 40 45
 Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg Thr
 50 55 60
 His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met His
 65 70 75 80
 Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His Pro
 85 90 95
 Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr Gly
 100 105 110
 Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe Glu
 115 120 125
 Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met
 130 135 140
 Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys Ile
 145 150 155 160
 Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met
 165 170 175
 Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu
 180 185 190
 Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Asn
 195 200 205
 Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys
 210 215 220
 Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu
 225 230 235 240
 Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val
 245 250 255
 Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu
 260 265 270
 Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val
 275 280 285
 Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe

290	295	300	
Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met	Gly Cys His Glu Ile		
305	310	315	
Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys	Leu Ser Lys Asp Asp	320	
325	330	335	
Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu	Asn Ala Ser Gly Leu		
340	345	350	
Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys	Arg Thr Gly Ser Ala		
355	360	365	
Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn	Ile Gly Tyr Ala Trp		
370	375	380	
Ile Val Ile Phe Gln Val Ile Thr Leu Glu	Gly Trp Val Glu Ile Met		
385	390	395	400
Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn	Phe Ile Tyr Phe Ile		
405	410	415	
Leu Leu Ile Ile Ser Glu Leu Ile His Leu	Val Met Pro Asp Cys Ser		
420	425	430	
Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln	Gly Asp Ser Leu Pro Gly		
435	440	445	
Val Ala Ala Glu Ser Leu Leu Arg Asp Ser Ser	Ser Ser Val Ile		
450	455	460	
Thr Asp Glu Ala Ala Ala Met Glu Asn Leu	Leu Ala Gly Thr Ser Lys		
465	470	475	480
Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala	Gly Ser Gln Val His Ser		
485	490	495	
Gln Ala Gln Gln Met Leu Gly Arg Gly Leu	Gly Pro Glu Ser Leu Glu		
500	505	510	
Thr Gly Glu Glu Pro His Ser Trp Ser Pro	Arg Ala Thr Arg Arg Trp		
515	520	525	
Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu	Pro Leu His Phe Met Gln		
530	535	540	
Ala Gln Val Gly Ser Phe Phe Met Ile Asn	Leu Cys Leu Val Val Ile		
545	550	555	560
Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg	Glu His Arg Leu Met Leu		
565	570	575	
Glu Gln Arg Gln Arg Tyr Leu Ser Ser Thr	Val Ala Ser Tyr Ala		
580	585	590	
Glu Pro Gly Asp Cys Tyr Glu Glu Ile Phe	Gln Tyr Val Cys His Ile		
595	600	605	
Leu Arg Lys Ala Lys Arg Arg Ala Leu Gly	Leu Tyr Gln Ala Leu Gln		
610	615	620	
Ser Arg Arg Gln Ala Leu Gly Pro Glu Ala	Pro Ala Pro Ala Lys Pro		
625	630	635	640
Gly Pro His Ala Lys Glu Pro Arg His Tyr	Pro Leu Thr Val Trp Glu		
645	650	655	
Ser Ile Leu Gly Arg Gln Ala Glu Glu	Cys Thr Leu Arg Ala Ala Ala		
660	665	670	
His Pro Ser Ser Gly Ala Ser His Pro Gly	Val Gly Ser Glu Glu Ala		
675	680	685	
Pro Glu Leu Cys Pro Gln His Ser Pro Leu	Asp Ala Thr Pro His Thr		
690	695	700	
Leu Val Gln Pro Ile Pro Ala Thr Leu Ala	Ser Asp Pro Ala Ser Cys		
705	710	715	720
Pro Cys Cys Gln His Glu Asp Gly Arg Arg	Pro Ser Gly Leu Gly Ser		
725	730	735	
Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser	Ser Ala Gly Gly		
740	745	750	

Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly Ala
 755 760 765
 Ser Ser Glu Leu Gly Lys Glu Glu Glu Glu Gln Ala Asp Gly
 770 775 780
 Ala Val Trp Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Ala Lys Leu
 785 790 795 800
 Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met Ala
 805 810 815
 Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln Ala
 820 825 830
 Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln Asn Pro Asp
 835 840 845
 Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro Ser
 850 855 860
 Pro Gly Gln Gly Val Leu Ser His Pro Val Thr Pro Pro His Thr Ala
 865 870 875 880
 Pro Trp Arg Met Glu Thr Gly Lys Gln Gly His Gly Cys Glu Gly
 885 890 895
 Pro Gly Gln Arg Ser Ser Asp Met Phe Ala Leu Glu Met Ile Leu Lys
 900 905 910
 Leu Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn Ile
 915 920 925
 Phe Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly Gln
 930 935 940
 Ala Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg Val
 945 950 955 960
 Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val Val
 965 970 975
 Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met
 980 985 990
 Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly Cys
 995 1000 1005
 Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg Lys
 1010 1015 1020
 Asn Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu
 1025 1030 1035 1040
 Thr Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser Thr
 1045 1050 1055
 Ser Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly Asn
 1060 1065 1070
 Tyr Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln
 1075 1080 1085
 Ala Glu Val Thr Val Val Leu Ala Glu Glu Ala Pro Pro Gln Gly Leu
 1090 1095 1100
 Arg Lys Thr Gly Arg Gly Arg Gly Leu Asp Gly Gly Gly Leu Gln
 1105 1110 1115 1120
 Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly Val Ala Asp
 1125 1130 1135
 Glu Val Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser Ser
 1140 1145 1150
 Ser Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser
 1155 1160 1165
 Gly Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His Leu
 1170 1175 1180
 Asp Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala
 1185 1190 1195 1200
 Gly Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala

1205	1210	1215
Leu Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser Tyr		
1220	1225	1230
Asp Gln Arg Ser Leu Val Gly Gly Leu Arg Ala Thr Ala Gly Val Gln		
1235	1240	1245
Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp Val Cys Leu Trp Gly		
1250	1255	1260
Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg Ser Ser Tyr		
1265	1270	1275
Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser Ser		
1285	1290	1295
Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser Leu		
1300	1305	1310
Leu Ser Ala Glu Arg Gly Gly Ala Arg Val Cys Glu Val Ala Ala		
1315	1320	1325
Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala His		
1330	1335	1340
His Val His His Gly Pro His Leu Ala His Arg His Arg His His Arg		
1345	1350	1355
Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser Val Asp Leu Ala Glu Leu		
1365	1370	1375
Val Pro Ala Val Gly Ala His Pro Arg Ala Ala Trp Arg Ala Ala Gly		
1380	1385	1390
Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala		
1395	1400	1405
Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp		
1410	1415	1420
Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Ala Glu Gly Asp Leu		
1425	1430	1435
Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp		
1445	1450	1455
Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu		
1460	1465	1470
Asn Arg Leu Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly Lys		
1475	1480	1485
Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg Gln		
1490	1495	1500
Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe Ile		
1505	1510	1515
Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu Ala		
1525	1530	1535
Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe Thr		
1540	1545	1550
Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly Leu		
1555	1560	1565
Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp		
1570	1575	1580
Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu Ala		
1585	1590	1595
Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg Leu		
1605	1610	1615
Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly Leu		
1620	1625	1630
Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly Asn		
1635	1640	1645
Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly		
1650	1655	1660

Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp Thr
 1665 1670 1675 1680
 Arg Asn Ile Thr Asn Arg Ser Asp Cys Met Ala Ala Asn Tyr Arg Trp
 1685 1690 1695
 Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser
 1700 1705 1710
 Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr Asn
 1715 1720 1725
 Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His Asn
 1730 1735 1740
 Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser Phe
 1745 1750 1755 1760
 Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys
 1765 1770 1775
 Cys Arg Gln His Gln Glu Ala Glu Ala Arg Arg Arg Glu Glu Lys
 1780 1785 1790
 Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu Pro
 1795 1800 1805
 Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met Cys
 1810 1815 1820
 Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu Asn
 1825 1830 1835 1840
 Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
 1845 1850

<210> 20
 <211> 567
 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (1)...(567)
 <223> Human alpha-1 partial sequence

<400> 20
 atg cgg atc ctg gtg aac ctg ctc ctg gac aca ctg ccc atg ctg ggg
 48
 Met Arg Ile Leu Val Asn Leu Leu Asp Thr Leu Pro Met Leu Gly
 1 5 10 15

aat gtc ctg ctg ctc tgc ttc ttt gtc ttc ttc acc ttt ggc atc ata
 96
 Asn Val Leu Leu Cys Phe Phe Val Phe Phe Thr Phe Gly Ile Ile
 20 25 30

ggt gtg cag ctc tgg gcg ggc ctg ctg cgt aac cgc tgc ttc ctg gag
 144
 Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
 35 40 45

gag aac ttc acc ata caa ggg gat gtg gcc ttg ccc cca tac tac cag
 192
 Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
 50 55 60

ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg tcg ggc gac
 240
 Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp
 65 70 75 80

 aat ggg ata atg ggc tgc cat gag atc ccc ccg ctc aag gag cag ggc
 288
 Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
 85 90 95

 cgt gag tgc tgc ctg tcc aag gac gac gtc tac gac ttt ggg gcg ggg
 336
 Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
 100 105 110

 cgc cag gac ctc aat gcc agc ggc ctc tgt gtc aac tgg aac cgt tac
 384
 Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
 115 120 125

 tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt gcc atc
 432
 Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile
 130 135 140

 agc ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag gtg atc
 480
 Ser Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile
 145 150 155 160

 act ctg gaa ggc tgg gtg gcg atc atg tac tac gtg atg gat gct ctc
 528
 Thr Leu Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu
 165 170 175

 tcc ttc tac aac ttc gtc tac ttc atc ctg ctt atc ata
 567
 Ser Phe Tyr Asn Phe Val Tyr Phe Ile Leu Leu Ile Ile
 180 185

 <210> 21
 <211> 188
 <212> PRT
 <213> Human

 <400> 21
 Arg Ile Leu Val Asn Leu Leu Asp Thr Leu Pro Met Leu Gly Asn
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 Val Leu Leu Leu Cys Phe Phe Val Phe Phe Thr Phe Gly Ile Ile Gly
 20 25 30
 Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu
 35 40 45
 Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro
 50 55 60
 Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp Asn
 65 70 75 80

Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly Arg
85 90 95
Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly Arg
100 105 110
Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr Tyr
115 120 125
Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile Ser
130 135 140
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile Thr
145 150 155 160
Leu Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu Ser
165 170 175
Phe Tyr Asn Phe Val Tyr Phe Ile Leu Leu Ile Ile
180 185

<210> 22
<211> 567
<212> DNA
<213> Rat

<220>
<221> CDS
<222> (1)...(567)
<223> Rat alpha-1 partial sequence

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Met Arg Ile Leu Val Asn Leu Leu Asp Thr Leu Pro Met Leu Gly
1 5 10 15
aac gtg ctc ctg ctc tgt ttc ttc gtc ttc atc ttc ggc atc att
96
Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile
20 25 30
ggc gtg cag ctc tgg gca ggc ctg cta cgg aac cgc tgc ttc ctg gaa
144
Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
35 40 45
gaa aac ttc acc ata caa ggg gat gtg gcc ctg ccc cct tat tac caa
192
Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
50 55 60
cca gag gag gat gac gag atg ccc ttt atc tgc tcc ctg act ggg gac
240
Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
65 70 75 80
aat ggc atc atg ggc tgc cac gag atc ccc cca ctg aag gag cag ggc
288
Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
85 90 95

cgg gaa tgc tgc ctg tcc aaa gat gat gtg tat gac ttc ggg gcg ggg

336

Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
100 105 110

cgc cag gac ctc aac gcc agc ggt ctg tgc gtc aac tgg aac cgc tac
384

Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
115 120 125

tac aac gtc tgc cgc acg ggc aac gcc aac cct cac aag ggc gcc atc
432

Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile
130 135 140

aac ttt gac aac att ggc tat gcc tgg att gtg att ttc cag gtg atc
480

Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile
145 150 155 160

act ctg gaa ggc tgg gtg gag atc atg tac tat gtg atg gac gca cat
528

Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His
165 170 175

tct ttc tac aac ttc atc tac ttc atc ctg ctt atc ata

567

Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
180 185

<210> 23

<211> 188

<212> PRT

<213> Rat

<400> 23

Arg Ile Leu Val Asn Leu Leu Asp Thr Leu Pro Met Leu Gly Asn
1 5 10 15

Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile Gly
20 25 30

Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu
35 40 45

Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro
50 55 60

Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp Asn
65 70 75 80

Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly Arg
85 90 95

Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly Arg
100 105 110

Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr Tyr
115 120 125

Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile Asn
130 135 140

Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile Thr
145 150 155 160

Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His Ser
165 170 175
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
180 185

<210> 24

<211> 31

<212> PRT

<213> Human

<400> 24

Val Ile Ser Leu Glu Gly Trp Thr Asp Ile Met Tyr Tyr Val Gln Asp
1 5 10 15
Ala His Ser Phe Trp Asn Trp Ile Tyr Phe Val Leu Leu Ile Val
20 25 30

<210> 25

<211> 31

<212> PRT

<213> C. elegans

<400> 25

Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
1 5 10 15
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile
20 25 30

<210> 26

<211> 23

<212> PRT

<213> Human

<400> 26

Asn Ile Asn Leu Thr Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
1 5 10 15
Arg Ala Val Asn Arg Ile Pro
20

<210> 27

<211> 23

<212> PRT

<213> C. elegans

<400> 27

Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
1 5 10 15
Lys Ala Ile Asn Arg Val Pro
20

<210> 28

<211> 19

<212> PRT

<213> Human

<400> 28

Met Ala Val Ile Met Ile Asn Cys Val Thr Leu Gly Met Tyr Arg Pro
1 5 10 15

Cys Glu Asp

<210> 29
<211> 19
<212> PRT
<213> C. elegans

<400> 29
Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met Tyr Gln Pro
1 5 10 15
Cys Asp Asp

<210> 30
<211> 23
<212> PRT
<213> Human

<400> 30
Leu Thr Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Val
1 5 10 15
Asn Arg Ile Pro Ser Met Arg
20

<210> 31
<211> 23
<212> PRT
<213> C. elegans

<400> 31
Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu
1 5 10 15
Ser Arg Phe Glu Gly Met Arg
20

<210> 32
<211> 41
<212> PRT
<213> Human

<400> 32
Pro Thr Ile Ile Arg Val Met Arg Val Leu Arg Ile Ala Arg Val Leu
1 5 10 15
Lys Leu Leu Lys Met Ala Lys Gly Ile Arg Ser Leu Leu Asp Thr Val
20 25 30
Gly Glu Ala Leu Pro Gln Val Gly Asn
35 40

<210> 33
<211> 40
<212> PRT
<213> C. elegans

<220>
<221> VARIANT
<222> (1)...(40)

<223> Xaa = Any Amino Acid

<400> 33

Pro Thr Leu Xaa Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu
1 5 10 15
Arg Leu Ile Lys Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu Met
20 25 30
Met Ser Leu Pro Ala Leu Phe Asn
35 40